

A:Molecule type: DNA
A:Residues: 1-1957 <CON>
A:Cross-references: EMBL:270690; PIDN:CAA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06c
A:Experimental source: strain 972h; cosmid c1f3
A:Genetics:
A:Gene: SPDB:SPAC1F3.06c
A:Map position: 1

Query Match 16.0%; Score 170.5; DB 2; Length 1957;
Best Local Similarity 23.6%; Pred. No. 0.048; Mismatches 92; Indels 43; Gaps 6;
Matches 58; Conservative 53;

OY 15 EENVNDRFLKNELDNVRRAQLSQKDEKRNDSQVITDLDTEENATVSLQALGKAE 74
DB 1386 EDNQLATNKLKQNDHLNQLRDLKEDVLEKESLIISLESISLNRQKSSLLDKNLE 1445
OY 75 -MLCSTLKKOMKYLEQOODETKOAOEAGRLRSKMTM-----EQIELL--LQSLP 123
DB 1446 HMLDTSRKNSLSMERIESINSLDDKSFELASAVEKLGALOKLHSESLSMENIKSQL 1505
OY 124 EVEEMIRDMGVGQSAVEOLAVYCVSLKKRYEN-----LKEARK 161
DB 1506 EAKKTIQ--VDESTIQELDHEITRASKNNYEGSKLNDKDSIIPDLSEBNTEQLNNLLAEKRS 1562
OY 162 ASGEVADKLRLKDLFSSRSKL-----QTVYSELDQAKLELSAOKDLQSDAKELMSLKK 214
DB 1563 AVKRLSTEEKSEIILQFNLSRLADLEYHKSQVESELSRSKRLKSLTEIELQLAENELSLTT 1622
OY 215 KLTMLQ 220
DB 1623 RMLDLQ 1628

RESULT 3
A26655
myosin heavy chain [similarity] - slime mold (Dictyostellium discoideum)
N:Contains: myosin Arpase (EC 3.6.1.32)
C:Species: Dictyostellium discoideum
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 02-Feb-2001
C:Accession: A26655; A24728; S00250
R:Warrick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 9433-9437, 1986
A:Title: Conserved protein domains in a myosin heavy chain gene from Dictyostellium disc
A:Reference number: A26655; MUID:87092266
A:Accession: A26655
A:Molecule type: DNA
A:Residues: 1-2116 <MAR>
A:Cross-references: GB:M14628; GB:M11938; NID:g167834; PIDN:AAA33227.1; PID:g167835
R:DeLozanne, A.; Lewis, M.; Spudich, J.A.; Leinwand, L.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 6807-6810, 1985
A:Reference number: A24728; MUID:86016788
A:Accession: A24728
A:Molecule type: mRNA
A:Residues: 2035-2116
R:Wagle, G.; Noegel, A.; Scheel, J.; Gerisch, G.
FEBS Lett. 227, 71-75, 1988
A:Title: Phosphorylation of threonine residues on cloned fragments of the Dictyostellium
A:Reference number: S00250; MUID:88112226
A:Accession: S00250
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1734-1893 <RAG>
C:Comment: The rod domain is highly periodic, containing a pattern of 7-residue repeats
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; phos
F:1-818/Domain: globular head <HED>
F:89-747/Domain: myosin motor domain homology <MMOT>
F:179-186/Region: nucleotide-binding motif A (P-loop)
F:819-2116/Domain: alpha-helical rod <ROD>

Query Match 15.4%; Score 164.5; DB 2; Length 2116;

Best Local Similarity 25.4%; Pred. No. 0.11;
Matches 68; Conservative 56; Mismatches 87; Indels 57; Gaps 11;

OY 5 NKLFFDLAQDEENVLD-REFLKNELDNVRAQLSQND---KERDSQVITDLDTEENATVSLQALG 60
DB 852 DKLESLKDTESNVLDLQROLKAERETLKAQYSDALDALEAKRELEIIVEDESELSDEK 911
OY 61 ATTVSLQ-----QALGKAEMLCSTLKKOMKYLEQOODETKOAOEAGRLRS 106
DB 912 LALENLQNRKSVREKRVNDLEPELOEBOKLRLNTLEKLKKYEELEBKRVNDGSDPTIS 971
OY 107 KKKTMEOIELLQSLPEVEEMI---RDMGV-----GQSAVBOLAVCVS----- 148
DB 972 R---LEKIKDELQKEVEELTESFSESKDKGVLEKTRVRLQSELDDLTVRLDSEFTKDKSE 1028
OY 149 ---LKKRYENKLEARKA-SGEVADKLRLKDLFSSRSKTIQTVYSELDQ-----AKLELK 196
DB 1029 LTRQKKLEELQYOEVLAAETAQLAOE--AANKRLQGETYTELINERFNSQVARSNVE 1086
OY 197 SAOKDLQS---ADKEIMSLKKRLTMLQ 220
DB 1087 KSKTLESQLAVANNELEDEKKNRDALE 1114

RESULT 4
JH0720
tanablin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 21-Jul-2000
C:Accession: JH0720
R:Hemmati-Brivanlou, A.; Mann, R.W.; Harland, R.M.
Neuron 9, 417-428, 1992
A:Title: A protein expressed in the growth cones of embryonic vertebrate neurons defi
A:Reference number: JH0720; MUID:92398961
A:Accession: JH0720
A:Molecule type: mRNA
A:Residues: 1-1744 <HEM>
A:Cross-references: GB:M9387; NID:g214816; PIDN:AAA49966.1; PID:g214817
A:Experimental source: tadpole head
C:Keywords: intermediate filament

Query Match 15.3%; Score 163.5; DB 2; Length 1744;
Best Local Similarity 25.8%; Pred. No. 0.1;
Matches 60; Conservative 61; Mismatches 73; Indels 39; Gaps 9;

OY 12 AOEBENVLDREFLKNELDNVRAQLSQKDEKRNDSQVITDLDTEENATVSLQALG 71
DB 33 ALREEN---ELLRKREIHSLSRSKSEKRCMKKNHEEM-KLRDALDDGHRKV----- 80
OY 72 KAEMLCSTLKKOMKYLEQOODETKOAOEAGRLRSKMTMEOIELLQSL-----P 123
DB 81 QHEWVRDSIYEIEFVKRCLEBKQAREDAKKESESKKLEBEETRAOIMLKERIGOLEA 140
OY 124 EVEEMIRDMGVGQSAVEOLAVYCVSLKRYENLKEARKA--SGEVADKLRL--DLFSS-- 177
DB 141 ELEDILRHEEKKALME---ELASFQRLSEFRAVPAFVPVEDVDARLSEIMQGA 197
OY 178 ---RSKLTQVSELDQAKLELSAOKD-----LQSDKELMSLKKRLTMLQ 220
DB 198 EYKSEVSVLEAGLSESKENLRKVLSENNKONRLLOSIDKELVSLKMKKALE 250

RESULT 5
T42722
male-enhanced antigen-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T42722
R:kondo, M.; Sutoh, S.
DNA Seq. 7, 71-82, 1997
A:Title: Cloning and molecular characterization of cDNA encoding a mouse male-enhance
A:Reference number: 222242; MUID:97217683

A:Accession:TA2722
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1325 <R>
A:Cross-references: EMBL:D78270, NID:d1096175, PID:d1020389, PIDN:BAAL19612.1.1
A:Experimental source: strain C0-1
C:Function:
A:Description: supposed to play some role for spermatogenesis
C:Keywords: leucine zipper

Query Match Similarity	15.1%;	Score 161;	DB 2;	Length 1325;
Best Local Similarity	23.1%;	Pred No. 0.11;		
Matches 57; Conservative	48;	Mismatches 90;	Indels 52;	Gaps 7;

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OY 13 QEEENVDLREFLNKELD-----NVRALOSKDKERDSQVILIDLPTDLERNANTVSL 66
OY 966 REHNSIETLALAKREADVOLNINQVAVLORKEEEDROKOLQVAVLSLEKKEKEMVSL 10235
OY 67 QALGKA-----BMLCSLTKOMKRYLEQO---QDET 94
Db 1026 KEQMAAAIRIEAGNHRHFRKATLESEVKKELQAKENHVLQVTLQAEVDELDQIDGKHSGEI 10855
OY 95 KOAEERGRJRSKKKKTMEQJLELLQSLPVEVEIMIDMGVGSINVEQLAVYCVSLKREYE 154
Db 1086 AOFQTELEAEATQIQ-----LQCKQI--DEQMSQOPTGQEMEDKLWEIJDOKEREIQ 11355
OY 155 NUKERAKASGEVADLRKKDLFFSSRSKIQTVYSELDQAKLELKSAAQDLQSDADKEIYMSLK 214
Db 1136 SLKQQLDLTDEQOQ---KKELEGQVQLQTLIKSLELVAGDLEBTLQDKDKRMIDAKKXSELKN 11922
OY 215 KL-TMLQ 220
Db 1193 NMKTLILQ 1199

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RESULT 6
A40997
myosin heavy chain, striated adductor muscle - scallop (Aequipecten irradians)
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Aequipecten irradians
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: A40997; S13557
R:Niltray, L.; Goodwin, E.B.; Szent-Gyorgyi, A.G.
J:BIOL. Chem. 266:18465-18476, 1991
A:Title: Complete primary structure of a scallop striated muscle myosin heavy chain. See
A:Reference number: A40997; MUID:92011595
A:Accession: A40997
A:Molecule type: mRNA
A:Residues: 1-1938 <NT>
A:Cross-references: GB:X55714; NID:g5611; PIDN:CA439247.1; PID:g5612
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide b
F:86-763/Domain: myosin motor domain homology <MMOT>
F:176-183/Region: nucleotide-binding motif A (P-loop)
F:547-586/Region: actin binding #status predicted
F:653-675/Region: actin binding #status predicted
F:836-1938/Domain: coiled coil #status predicted <COI>
F:836-1276/Region: S2
F:1277-1938/Region: light meromyosin
F:1893/Binding site: ATP (Lys) #status predicted
F:1693,703/Active site: Cys #status predicted

Query Match	15.1%;	Score 160.5;	DB 1;	Length 1938;
Best Local Similarity	28.1%;	Pred. No. 0.17;		
Matches 56; Conservative	46;	Mismatches 70;	Indels 27;	Gaps 7.

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QY 10 DLAGEENVYLDRELKANEL-DNFR--AQLSQDKDKRDSQYIIDTLRPTLEENATYVS 65
   || :||| || :|| :||| :||| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 1055 DKSTQEVNEDLEVKRKELEENARRKAEALISLNSKLEBONLVSOLQRIKTELQARIIE 1114
   || :||| || :|| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 66 LQALGRKAEMLCTSLKQKMTLEBQDDQETQAOEDBGRLSRKKMTQETLELLLSQLEPEV 125

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Db      1115  LEEELAEFRNARAVEKORQRELELNEFELGERIDEGG-----ANSQJLELKKKE AEL 1168B
Qy      136  EEMIIDMGVGSAAVEOLAVYCVSLKEKEYELKARRASGEVADKILKDLFSSRSKIQTIVY 185
Db      1169  LKIRIDL---EASLQHEAQSIALRKHQD-----AANEMADQV-----DQLOKVK 1211B
Qy      186  SELDQAKLELTSQAQDLOS 204
Db      1212  SKLEKQKDKLTKREMDLES 1230

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Db 1212 SKLEKDKDLKREDDLES 1230

RESULT 7
T30171

C:Species: *Mus musculus* (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: J30171
R:Bouckson-Castaing, V.; Moudjou, M.; Ferguson, D.J.P.; Mucklow, M.; Belkaid, Y.; Millat, J. Cell Sci. 109, 179-190, 1996
A>Title: Molecular characterisation of nihelin, a new coiled-coil protein of the centrosome
A:Reference number: J20751; MUID:96431720
A:Accession: J30171
A>Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-2168 <BDU>
A:Cross-references: EMBL:U40342; NID:g1113864; PID:g1113865; PIDW:AAA83234.1
A:Experimental source: strain C57BL/6
A>Note: localised specifically in the pericentriolar matrix of the centrosome

Query Match	15.1%;	Score 160.5;	DB 2;	Length 2168;
Best Local Similarity	22.7%;	Pred. No. 0.19;		
Matches 58; Conservative	54;	Mismatches 90;	Indels 53;	Gaps 7.

QY	1	RIINKLEFDLAGEENVYDEFLKNTLDNVNROLQSOXOKERKDSQV11IDTLRDLTEEN	60
Db	1592	QTMERKL-----KKOVSIDKIKINOODDENIELSOKNSQNEE-----LKITINOL	1633
QY	61	ATVVSILQOALG-----KAEMICSTLKKOMKYLEPOODETKQAOE--EAGRILSRKMTMEOI	114
Db	1638	AEMLCQREBPQACSTSEKMEQENASLKEBIDHYKQVQSTVLSLEADLSIKLQTHNMEQ	1697
QY	115	ELLDSQRPVEYEMIR--DMQVGSANVEQLAVNVCYSLKKEEYULKARKASG-----	164
Db	1696	NLLKDELERLKLQRCOPDLSLQOKKNSVYLSITNEKLEKEVLSLEELSCADKLAESSL	1757
QY	165	-----EYADLRKDRPSSRSKQIQTAVSELDQAKLELKSQKDLQ-----	203
Db	1758	LEHRITATKQOETAMEBQSELSKQLAVSQAKYODLEDVQNNLOMAELIESLDQVTRQE	1811
QY	204	---SADKETMSLKKUL	216
Db	1818	KEAVKQEVMSLHROL	1832

RESULT 8

myosin heavy chain - Entamoeba histolytica
C:Species: Entamoeba histolytica
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C:Accession: T18296

submitted to the EMBL Data Library, February 1997
A:Reference number: Z18865
A:Accession: T18296
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-2139 <GUI>
 A:Cross-references: EMBL:U03534; NID:g1850912; PID:g1850913; PIDN:AMB48065.1
 C:Genetics:
 A:Gene: mhca
 C:Superfamily: myosin heavy chain; myosin motor domain homology

F:91-780/Domain: myosin motor domain homology <MMO>

Query Match 15.0%: Score 159.5; DB 2; Length 2139;
Best Local Similarity 24.0%: Pred. No. 0.21;
Matches 60; Conservative 49; Mismatches 96; Indels 45; Gaps 7;

QY 5 NKLFDL--AOEENVLNREFLNELDNVRAQLSQKDEKRDSDVI-----ID 50
DB 1144 NKIBEDLNNAQRKIKLEDEDTTKGA--DV-SQYLQKQKEVEESQJAKKQOEKEATGNVYK 1200
QY 51 TLRDITLEERNATVVSLOQALGKAEMLCSTLKKOMKYLEQOODETKQAOEEAGRLSKMKT 110
DB 1201 NKEKIKKEKELEIOSLOEKLEDETEVEKEDAEKKKEIEK---EMKALQEEKENVESSKNS 1257
QY 111 MEQIEELLQSQLPVEEEMIRDMGVQGSVAVEQIAYVCSLKEKEYELKPKARKASGVAAKL 170
DB 1258 TEKDKKKLEDDNKDKTDKTDNDEKTLAKAKDLEKQLEVDNHNKRAVADADELK 1317
QY 171 R----KDLFSSRSKLQ-----TVSELDQAKLELKSACKDLSA 205
DB 1318 KAQSKKELNSLKAELFALTAKKSVESKNKDSSEKAKALSEIDQANKELKNIGADLKKA 1377
QY 206 DKEIMSLKK 215
DB 1378 TADLQEANEK 1387

RESULT 9

S67593
N:Alternate protein USO1 - yeast (Saccharomyces cerevisiae)

C:Alternate names: protein D2552; protein YDL058w

C:Species: Saccharomyces cerevisiae

C:Date: 12-Jul-1996 #sequence.revision 12-Jul-1996 #text.change 21-Jul-2000

C:Accession: S67593; A38455; S30782

R:Bioecker, H.; Brandt, P.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67593

A:Accession: S67593

A:Molecule type: DNA

A:Residues: 1-1790 <BL0>

A:Cross-references: EMBL:Z74106; NID:91431056; PID:e253003; PID:91431059; MIPS:YDL058w

A:Experimental source: strain S288c

R:Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M.

J. Cell Biol. 113, 245-260, 1991

A:Title: A cytoskeleton-related gene, USO1, is required for intracellular protein transp

A:Reference number: A38455; MUID:91185402

A:Accession: A38455

A:Molecule type: DNA

A:Residues: 1-389, '392-724, 'S', '726-1790 <NAK>

A:Cross-references: GB:X54378; NID:94777; PIDN:CA38253.1; PID:94778

A:Note: the authors translated the codon ACT for residue 768 as Ile

R:Hostetter, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E.

submitted to the EMBL Data Library, February 1993

A:Description: An integrin analogue in Saccharomyces cerevisiae.

A:Reference number: S30782

A:Accession: S30782

A:Molecule type: DNA

A:Residues: 71-846, 'E', '848-923, 'K', '925-1252, 'I', '1254-1318, 'V', '1320-1460, 'S', '1462-1580, 'S

A:Cross-references: EMBL:L03188

C:Genetics:

A:Gene: SGD:USO1; INT1

A:Cross-references: SGD:S0002216; MIPS:YDL058w

A:Map position: 4L

C:Keywords: coiled coil; transmembrane protein

F:326-342/Domain: transmembrane #status predicted <TM1>

F:394-410/Domain: transmembrane #status predicted <TM2>

F:617-633/Domain: transmembrane #status predicted <TM3>

Query Match

Best Local Similarity 23.7%: Pred. No. 0.19;
Matches 61; Conservative 57; Mismatches 85; Indels 54; Gaps 9;

QY 1 RTIINKLFFDLA0---EEENVLDREFLK-----NELDNVRAQLSQKDEKRDSDVI 48
DB 1369 RKLNEGSSITTOEYSEKINFLLEDELIRLQENELKAKEDINTSEL-EKSLSDN----- 1423
QY 49 IDTLRDITLEERNATVVSLOQAL-----GKAEMLCSTLKKOMKYLEQOODETKQAOEE 100
DB 1424 -----ELLEEKQNTKSLQDELILSVKDKITRNDEKLSIFERNKRDLESLKEQIRAAQES 1478
QY 101 AGRLSKMKTMEQIEELLQSQLPVEEEMIRDMGVQGSVAVE---QLAVYVCSLKEKEYENL 156
DB 1479 KAKVEEGKLKLEESSKREKALEKSKEMMKRL---ESTIESNETLSSMETIKRSDEKL 1535
QY 157 KEARKASGEVADKLR-----KDLFSSRSKLQTVY---SELDQAKLELKSQAQ 199
DB 1536 ESKKSAEEDIKNQLQHEKSDLSIRNESKDIIEELKSLRLIANSGSBELTVKQELNNAQ 1595
QY 200 KDLSQADKEIMSLKKL 216
DB 1596 EKIRINAEENTVLSKSL 1612

RESULT 10

S06006
myosin beta heavy chain, cardiac muscle [similarity] - rat

N:Contains: myosin ATPase (EC 3.6.1.32)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1993 #sequence.revision 31-Dec-1993 #text.change 19-Jan-2001

C:Accession: S06006; S07536; I67441; A02989

R:Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.

Nucleic Acids Res. 17, 7529-7530, 1989

A:Title: Complete nucleotide sequence of full length cDNA for rat beta cardiac myosin

A:Reference number: S06006; MUID:90016823

A:Accession: S06006

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-1935 <RA>

A:Cross-references: EMBL:X15939; NID:956656; PIDN:CAA34065.1; PID:956657

R:McNally, E.M.; Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.

J. Mol. Biol. 210, 665-671, 1989

A:Title: Full-length rat alpha and beta cardiac myosin heavy chain sequences. Compari

A:Reference number: S07535; MUID:90133919

A:Accession: S07536

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-950, 'RK', '953-1935 <MCN>

R:Mahdavi, V.; Lompre, A.M.; Chambers, A.P.; Nadal-Ginard, B.

Eur. Heart J. 5, 181-191, 1984

A:Title: Cardiac myosin heavy chain isozymic transitions during development and under

A:Reference number: I53305; MUID:85179510

A:Accession: I67441

A>Status: translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1871-1935 <RES>

A:Cross-references: GB:M32698; NID:9205598; PIDN:AAA41659.1; PID:9205599

R:Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B.

Nature 297, 659-664, 1982

A:Title: Molecular characterization of two myosin heavy chain genes expressed in the

A:Reference number: A02988; MUID:82220036

A:Accession: A02989

A:Molecule type: mRNA

A:Residues: 1524-1528, 'V', '1530, 'R', '1532-1730, 'H', '1732-1783, 'K', '1785-1850, 'N', '1852-185

A:Cross-references: GB:J00752; NID:9205577; PIDN:AAA41654.1; PID:9205578

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl

F:178-185/Domain: myosin motor domain homology <MMOT>

F:148-185/Region: nucleotide-binding motif A (P-loop)

F:548-585/Region: actin binding #status predicted

F:655-677/Region: actin binding #status predicted

F:839-1935/Domain: coiled coil #status predicted <COI>

F:839-1279/Region: 52

F:1280-1935/Region: 1935

F:129/Modified site: N6,N6-trimethyllysine (Lys) #status predicted

F:184/Binding site: ATP (lys) #status predicted
F:695,705/Active site: Cys #status predicted

Query Match 14.7%; Score 158.5; DB 1; Length 1935;
Best Local Similarity 20.1%; Pred. No. 0.22;
Matches 62; Conservative 60; Mismatches 87; Indels 89; Gaps 9;

QY 1 RTIINKLFPLDQEEENVLDR-----EPLK----- 25
DB 1129 RAKVEKRLSDLSRELEPISRELEAGATSVQIEMNKKREAEQKMRDLDEATLQHEAT 1188
QY 26 -----NELDNVRAQLSOKDKERDSQVIIDTLTDEERNATVVSLOQA 69
DB 1189 AALARKKHADSVALGQIDNLQVHKOKLEKSEFKLEDDVYSNMHQ-----IIRA 1241
QY 70 LGKAEMLCSTLKKOMKYLEQOODETKQAQAEAGRLRSKMT-----MEQIEPLLQSQ 121
DB 1242 KANLEKMCRTLEDQMNHRSKAEFTQSVNDLTRQAKLQTEENGELSRLQDEKALISQ 1300
QY 122 LP-----EVEEMIRDMGVGGSVAVQQLAVYCVSLKKEVENLKEAKAGSEV 166
DB 1301 LTRGKLYTQOLEDLKRQLEEVAKKNAHALQSAHRHDCDLREQYEETEAKAELOQV 1360
QY 167 ADLRKDLFSSRSKIQT-----VSELDQAKLELKSQOKDLOSADKEIMSLKKTLMLO 220
DB 1361 LSKANSEVAQMKRTYEDAIQRTLELEBAKKL--AQR-LQDAEAVAVAKCSSLE 1415

RESULT 11
A55913

transcytosis-associated protein p115 - rat

C:Species: Rattus norvegicus (Norway rat)
C>Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 05-Nov-1999

C:Accession: A55913

R:Barroso, M.; Nelson, D.S.; Szul, E.

Proc. Natl. Acad. Sci. U.S.A. 92, 527-531, 1995

A:Title: Transcytosis-associated protein (TRP)/p115 is a general fusion factor required

A:Reference number: A55913; MUID:95132633

A:Accession: A55913

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-959 <BAR>

A:Cross-references: GB:U15589; NID:9558474; PIDN:ANC52151.1; PID:9558475

C:Keywords: membrane fusion; membrane trafficking

Query Match 14.7%; Score 156.5; DB 2; Length 959;

Best Local Similarity 20.1%; Pred. No. 0.14;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

QY 15 EENVLDREFLK--NELDNV--RAQLSOKDKERDSQVIIDTLRPTLEERNATVVSLOQA 70
DB 605 EYMFDFHEFTKLVELEGVITKATYKSSSEDKKEEV-----KRTLEQHDNIYTHYKNVI 659
QY 71 GKAEMLCSTLKKOMKYLEQOODE-----TKQAQ----- 98
DB 660 REQDLQLEELKQVSTLKQNEQLOQTAVTQOASIQQHKDOYNILKYOLGKDNHQS 719
QY 99 -----EAGRLSKMTMEQIELLSQSLPEVEEMTRDM-----GVGGSVAV--- 139
DB 720 DGAQVNGIQPEIRLREIREIELRSHQVLLSQLAEKDTYENLRSSVGSMSQDALATC 779
QY 140 -----EQLAVY----- 145
DB 780 SPRDAEQVAELKQELSAKLSQCSQSLITRQLQTEENRELQOARAEFLAKSVPEGESELYT 839
QY 146 -----CVSLKKEVENLKEAKAGSEVADLRKDLFSSRSKLTQVYSELQAKLEL 195
DB 840 AAKTTDVEGRSLALQETKEKLEIKALSEERTSIQKOLQSSNSTIATLQTEKQKLYLEV 899
QY 196 KSAQKD-----LOSADKEIMSLKKT 216

DB 900 TDSKKEQDILLVLLADQKILSLKSKL 927

RESULT 12

T24635

hypothetical protein T07C4.10a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000

C:Accession: T24635; S41023

R:Buck, D.

submitted to the EMBL Data Library, February 1995

A:Reference number: T24635

A:Accession: T24635

A:Status: preliminary; translated from GB/EMBL/DDDBJ

A:Molecule type: DNA

A:Residues: 1-1138 <WIL>

A:Cross-references: EMBL:248055; PIDN:CAA8136.1; GSPDB:GN00021; CESP:T07C4.10a

A:Experimental source: clone T07A5

R:Berts, M.

submitted to the EMBL Data Library, January 1994

A:Reference number: S41014

A:Accession: S41023

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 895-1138 <BER>

A:Cross-references: EMBL:229443

C:Genetics:

A:Gene: CESP:T07C4.10a

A:Map position: 3

A:Introns: 16/1; 124/3; 146/3; 204/1; 311/3; 358/3; 615/3; 900/2; 961/3; 1008/2; 1110

Query Match 14.7%; Score 156.5; DB 2; Length 1138;

Best Local Similarity 24.7%; Pred. No. 0.16;
Matches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;

QY 1 RTIINKLFPLDQEEENVLDRF--LKNELDNVRAQL-----SOKDKER 43
DB 544 KTIYKENVY-LSEKQVLESEINLKNELDNMAVKLNQSHQVAGLNEKISEERRRRKKQ 602
QY 44 DSQVIIDTLRPTLEERNATVVSLOQALGKAEML--CSTLKKOMKYLEQOODETKQAQEEA 101
DB 603 DADV-----TRLDEQOKL--LREAQDSALLEEVQKGRREIDHLRQLAHOSSEAGSV 654
QY 102 GRLSKAKTMEQIELLSQSLPEVEEMIRDMGVGGSVAVQQLAVYCVSLKKEVENLKEAK 161
DB 655 GQLDQOKLAESEREHYLLQLELELERYVMKMERD-----LDGRIBGYIRSEA 697
QY 162 ASGEVAKLRKDLFSSRSKLTQVYSELQAKLELKSQOKDLOSADKEIMSLKKT 216
DB 698 ANNELERLKRDTAEQKEKLEA-----MEKARSKDLELAD-----LTRKL 738

RESULT 13

PC4035

cell-cycle-dependent 350K nuclear protein - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 08-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000

C:Accession: PC4035

R:Li, Q.; Ke, Y.; Kapp, J.A.; Fertig, N.; Medsger Jr., T.A.; Joshi, H.C.

Biochem. Biophys. Res. Commun. 212, 220-228, 1995

A:Title: A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain suff

A:Reference number: PC4035; MUID:95336446

A:Accession: PC4035

A:Molecule type: DNA

A:Residues: 1-1017 <LIQ>

A:Cross-references: GB:U25725; NID:9818866; PIDN:AAA86889.1; PID:9818867

A>Note: repeat 15-160 and 200-340

C:Comment: This protein contains a coiled-coil and a globular domain at the carboxy-t

C:Keywords: nucleoprotein; phosphoprotein
F:45/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #s
F:825,826,838/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #st
F:908,909/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status


```
QY      178 RSKLQT---VSELDQAKLELKSAQKDLQSADKEIMSLKKLLTMLQ 220
        |:|:|         |::||:|   ||:| |:| :|:| :|:| :|:|
Db     1375 RTKYETDAIORTTEELFEAAKKL--AQR-LQDAEEHVAVNKACASLE 1418
```

RESULT 17

N:Contains: myosin, skeletal muscle, embryonic - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
 C:Accession: A24922; A22538; B24263
 R:Strehler, E.E.; Strehler-Pager, M.A.; Perliard, J.C.; Periasamy, M.; Nadal-Ginard, B.
 J. Mol. Biol. 190, 291-317, 1996
 A:Title: Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy
 A:Reference number: A24922; MUID:87060988
 A:Accession: A24922
 A:Molecule type: DNA
 A:Residues: 1-1940 <STR>
 A:Cross-references: GB:X04267; GB:X05004; NID:g56658; PIDN:CAA27817.1; PID:g1619328
 R:Strehler, E.E.; Mandavji, V.; Periasamy, M.; Nadal-Ginard, B.
 J. Biol. Chem. 260, 468-471, 1985
 A:Title: Intron positions are conserved in the 5' end region of myosin heavy-chain genes
 A:Reference number: A22538; MUID:85080119
 A:Accession: A22538
 A:Molecule type: DNA
 A:Residues: 1-168 <STR2>
 A:Cross-references: GB:I200370; GB:M10135; NID:g205580; PIDN:AAA41655.1; PID:g554476
 R:Periasamy, M.; Wydro, R.M.; Strehler-Pager, M.A.; Strehler, E.E.; Nadal-Ginard, B.
 J. Biol. Chem. 260, 15856-15862, 1985
 A:Title: Characterization of cDNA and genomic sequences corresponding to an embryonic my
 A:Reference number: A24263; MUID:8605474
 A:Accession: B24263
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1358-1490, 'G' <PER>
 A:Cross-references: GB:U03468; NID:g205573; PIDN:AAA41652.1; PID:g205574
 A:Experimental source: clone pMHC-72
 C:Genetics:
 A:Introns: 68/3; 116/3; 169/1
 A>Note: The list of intron positions may be incomplete
 C:Superfamily: myosin heavy chain; myosin motor domain
 C:Keywords: actin binding; ATP; coiled coil; hydrophase; methylated amino acid; muscle co
 F:89-767/Domain: myosin motor domain homology <MMOT>
 F:179-186/Region: nucleotide-binding motif A (P-loop)
 F:349-586/Region: actin binding #status predicted
 F:656-678/Region: actin binding #status predicted
 F:840-1940/Domain: coiled coil #status predicted <COI>
 F:840-1280/Region: S2
 F:1281-1940/Region: light meromyosin
 F:130/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
 F:183/Binding site: ATP (Lys) #status predicted
 F:696/706/Active site: Cys #status predicted

Query Match	14.58	Score 155	DB 1	Length 1940
Best Local Similarity	23.88	Pred. No.	0.54	
Matches 53	Conservative 51	Mismatches 83	Indels 36	Gaps 7

QY	24	LKNELNVRALSDKDKRKRDSQYIIDPLRDTLEERNATVVSLODALGKAMLCSTLKKQ	83
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	1204	LAEOIDNQRVKOKLEKKESEFKLEIDLSSVE-----SVSKSKANLEKIRITLEDQ	1256
QY	84	MKYLEOODDETKOA-----OEAGRLRSKMKMTMEQIELL-----OSQLPEVEEM	128
		: : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	1257	LSEARGKMEEFQRSISELTQKSRLOTFAGELSRLEKESITVSOLSKSAFTQOQIEEL	1316
QY	129	IRDMGVGSAVEQLAVY-----CVSLKKEYENLKEARKASGEVADRLKRDLEFSSRSKL	181
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	1317	KRQLEEFKKAKNALHAHQSSRHDCDLLREQYEEEOEBKALQRLRLSKANSEVAMQRTKY	1376
QY	182	QT---VYSELDOAKLELKSQKDLQASADKEIMSLKKKLTLMQ	220

```

      :| ||::|| :| ||: || ::::: :| :| :
Db 1377 ETDAIQRTTEELFAKKL--AQR-LQDSEEQVAVNACASLE 1416

```

RESULT 18

myosin heavy chain II - Acanthamoeba castellanii
 N:Contains: myosin ATPase (EC 3.6.1.32)
 C:Species: Acanthamoeba castellanii
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
 C:Accession: A27224
 R:Hammer III, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.
 J. Cell Biol. 105, 913-925, 1997
 A:Title: Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle
 A:Reference number: A27224; MUID:87308395
 A:Accession: A27224
 A:Molecule type: DNA
 A:Residues: 1-1509 <NAM>
 A:Cross-references: GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID:g5585; PTDN:CA668
 C:Genetics:
 A:Introns: 69/3; 119/3; 181/2
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; ATP; coiled coil; hydrolyase; methylated amino acid; nucleoside
 F:92-775/Domain: myosin motor domain homology <MOM>
 F:182-189/Region: nucleotide-binding motif A (P-loop)
 F:544-576/Region: actin binding #Status Predicted
 F:660-682/Region: actin binding #Status Predicted
 F:848-1227/Domain: coiled coil #status predicted <COI>
 F:1228-1247/Domain: hinge <HIN>
 F:1248-1482/Domain: coiled coil #status predicted <CO2>
 F:1483-1509/Domain: carboxyl-terminal <CBT>
 F:133/Modified site: N6,N6,N6-trimethyllysine (lys) #status predicted
 F:188/Binding site: ATP (lys) #status predicted

Query Match	14.5%	Score 154.5;	DB 1;	Length 1509;
Best Local Similarity	25.8%	Pred. No. 0.28;		
Matches 69; Conservative	52;	Mismatches 91;	Indels 55;	Gaps 7;

[illegible]

RESULT 19
B75150
chromosome segregation protein (smc1) PAB2109 - *Pyrococcus abyssi* (strain Orsay)
C:Species: *Pyrococcus abyssi*
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: B75150
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: *Pyrococcus abyssi* genome sequence: Insights into archaeal chromosome s
A:Reference number: A75001
A:Accession: B75150
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-1177 <KAM>
A:Cross-references: GB:A1248284, GB:A1096836, NID:g5457730, PIDN:CAB49281.1, PID:g5457799
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2109
C:Superfamily: chromosome segregation protein SKC1

Query Match	14.4%;	Score 154;	DB 2;	Length 1177;
Best Local Similarity	22.9%;	Pred. No. 0.23;		
Matches	57;	Conservative	61;	Mismatches 87;
				Indels 44;
				Gaps 10;

Qy	6	KLFDFDLOEENSVNDRLEKLEEDNVAQLOXNDKERDSQVYIIDTLPDLEERNATVYS	65
		: :	
Db	178	KALOELKQAEENLARVDLLIRE---VKQLODKLEKERNDLARYID-LKERLEBARVELI-	232
		: :	
Qy	66	LOQALGKAEMCSTLKQOMKYLTCOOOETKQAOOE---AGRLSKMKWTQEOJIELLOS-	120
		: :	
Db	233	---LGEIKKVESEIKGNDERIERIEKEIEKEIEKLEIKELIYRKRELEKEVEEDLIEKE	288
		: :	
Qy	121	-----OLPEVEEHI-----RDMGVGQSAVDQLAVYCVSLKKEEYEN-LKARRASGE	165
		: :	
Db	289	SSEBALKTIREIGENSKINILAKNIEIAKLEDEAOIRLIKAKDEIKYLSIEIEKSKGA	348
		: :	
Qy	166	VA-----DKLRKDDFSSRSKLOTQVSELDQ---AKLELSAKODLOSADKEIMS	211
		: :	
Db	349	IARNGKREKREALNKNI-KELIEERKRLVVKJGEIDRFPAVARREEDNVYKLELNAARSYLE	407
		: :	
Qy	212	LKKKITLMQ 220	
		: :	
Db	408	NEADIKRLE 416	

RESULT 20
T22976
hypothetical protein F59A2.6 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T22976; T23157
R:Lightning, J.
submitted to the EMBL Data Library, June 1994
A:Reference number: Z19645
A:Accession: T22976
A:Status: preliminary; translated from GR/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-1133 <MI>
A:Cross-references: EMBL:Z34801; PID:CAA84332.1; GSPDB:GN00021; CESP:F59A2.6
R:Burton, J.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19700
A:Accession: T23157
A:Status: preliminary; translated from GR/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-1133 <MI2>
A:Cross-references: EMBL:Z66514; PID:CAA91344.1; GSPDB:GN00021; CESP:F59A2.6
C:Experimental source: clone K01A11
C:Genetics:
A:Gene: CESP:F59A2.6
A:Map position: 3
A:Insertions: 13/2; 43/3; 107/3; 413/3; 492/3; 567/3; 635/3; 710/3; 738/3; 795/2; 1008/3; 1

```

Query Match      14.4%  Score 153.5;  DB 2;  Length 1133;
Best Local Similarity 25.0%;  Pred. No. 0.24;
Matches 60;  Conservative 62;  Mismatches 77;  Indels 41;  Gaps 10;

QY  13 QEEFVLT--DREFFLKNEIDNVAQLSKQDKERPS-QVIITLRLDTLEERNATVYS----- 65
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  93 ESKKVLVESEKQAFENKEQEREREDLAKAMERKLNSEQNIIDVEYTKKLQSESEVYLAAGA 152
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY  66 ---LQALGKAEMLCTSLTKKQMKYIEQOODETKQAQEEAGRLRSKMTK-----EQ 113
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

```

[illegible]

RESULT 21

160K golgi antigen - human (fragment)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000

R;Fritzler, M.J.; Hamel, J.C.; Ochs, R.L.; Chan, E.K.L.
 J Exp Med 178 49-62 1993

A;Title: Molecular characterization of two

A:Accession: JH0820
A:Molecule type: MR

A;Residues: 1-379 <FRI>
A;Cross-references: EMBL:P06148: NID:q306783: PIDN:AAA35921.1: PID:q553309

A/Note: this protein has alpha-helical structure with beta sheet regions

F;67-73/Region: proline-rich

F;419-455/Region: leucine zipper motif

Query Match	Similarity	14.3%	Score 152.5	DB 2	Length 579
Best Local	Similarity	25.0%	Pred. No. 0.13		
Matches	Conservative	42	Mismatches	86	Indels 37; Gaps 6
QY	13 GEEENVLDREFPKNELD-----NVRACQSDKDEKRSQSVITDTLDTLLEERNATVSL	66			
DB	363 REHNSILEETALAKREADLVQMLQVAVLQKRKEEDRQKHLVQALQASLEKEKEVNSL	422			
QY	67 QOALCKAEMLCSTLKKOMKYLEQODEFK-----QAOEACRLSKKMKTME-	112			
DB	423 KEQVAARKEVAGHNRHNFPAASLEISEYKKELQAKENHLQYKQALAEADDQIREGKHSQEI	482			
QY	113 ---QIQL-----LLOSQLEPEVEEMIRDMGVGQSAVEQALAVVYCSLAKKENLKEARK	161			
DB	483 AQQFQELMAEARQQLDILQQL---DEQLSKQVGVNGEMENMLKWEVDQKRELTQSLQQLQD	539			
QY	162 ASGEVADKLRKDLFSSRSKRLQTVYSELDAQLELKSQKD	201			
DB	540 LTEQDQ---RKLEGLQQLDLQNVKSELLEAAQDLSLMTQD	576			

RESULT 22

myosin beta heavy chain, cardiac and skeletal muscle - human

C;Species: Homo sapiens (man)

C;Accession: A37102; S12733; A94224; B28908; A24997; A27858; I54254; S12458

Genomics 8, 194-206, 1990

A;Reference number: A37102; MUID:91065634
A;Accession: A37103

A: Molecule type: DN
A: Residues: 1-1935

R: Iw. C.C.: Sole M.T.: Yamauchi-Takahara K.: Keljam B.: Anderson D.H.: Jin T.:
A; Cross-references: GB:M5/965; GB:M30603; NID:gl/950/; PIDN:AAA5183/.1; PID:gl/9508;
A; Cross-references: GB:M5/965; GB:M30603; NID:gl/950/; PIDN:AAA5183/.1; PID:gl/9508;

A:Title: Complete sequence and organization of the human cardiac beta-myosin heavy chain
Nucleic Acids Res. 18, 3647-3651, 1990

A; Reference number: S12/33; MOID: 90301498

A:Accession: S12733
A:Molecule type: DNA
A:Residues: 1-106, 'E', 108-671, 'LYH', 675-857, 'A', 859-941, 'NV', 944-1123, 'A', 1125-1158, 'C',
A:Cross-references: EMBL:X52889; NID:929726; PIDN:CAA37068.1; PID:929727
R:Yamauchi-Takahara, K.; Sole, M.J.; Llew, J.; Ing, D.; Llew, C.C.
Proc. Natl. Acad. Sci. U.S.A. 86, 3504-3508, 1989
A:Title: Characterization of human cardiac myosin heavy chain genes.
A:Reference number: A94224; MUID:89264452
A:Accession: A94224
A:Molecule type: DNA
A:Residues: 1-87, 'Q', 89-106, 'E', 108-177; 1325-1702, 'DR', 1705-1786, 1788-1803, 'E', 1804-1933
R:Yamauchi-Takahara, K.; Sole, M.J.; Llew, J.; Ing, D.; Llew, C.C.
Proc. Natl. Acad. Sci. U.S.A. 86, 7416-7417, 1989
A:Contents: annotation; erratum
A:Reference number: A94226
A:Title: Molecular cloning and characterization of human cardiac alpha- and beta-form my
human atrium.
A:Reference number: A92770; MUID:88299163
A:Accession: B28908
A:Molecule type: mRNA
A:Residues: 1412-1518, 'R', 1520-1574, 'NV', 1577-1935 <KUR>
A:Cross-references: GB:M21665
A:Note: the authors translated the codon AGC for residue 108 as Arg
R:Lichter, P.; Umeda, P.K.; Levin, J.E.; Vosberg, H.P.
Eur. J. Biochem. 160, 419-426, 1986
A:Title: Partial characterization of the human beta-myosin heavy-chain gene which is exp
A:Reference number: A24997; MUID:87030293
A:Accession: A24997
A:Molecule type: DNA
A:Residues: 682-721, 975-1112, 1854-1935 <LIC>
A:Cross-references: GB:X04627
R:Saez, L.J.; Gianola, K.M.; Mcnally, E.M.; Feghali, R.; Eddy, R.; Shows, T.B.; Levinand
Nucleic Acids Res. 15, 5443-5459, 1987
A:Title: Human cardiac myosin heavy chain genes and their linkage in the genome.
A:Reference number: A93659; MUID:87260010
A:Accession: A27858
A:Molecule type: DNA
A:Residues: 1854-1865, 'A', 1867-1935 <SAE>
A:Cross-references: GB:X05631; GB:Y00362; NID:934664; PIDN:CAA29119.1; PID:g34644
R:Dielerich, K.W.; Elsele, I.; Ried, T.; Jaenicke, T.; Lichter, P.; Vosberg, H.P.
Hum. Genet. 81, 214-220, 1989
A:Title: Isolation and characterization of the complete human beta-myosin heavy chain ge
A:Reference number: I54254; MUID:89154425
A:Accession: I54254
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 653-720 <RES>
A:Cross-references: GB:M27636; NID:g179511; PIDN:AAA79019.1; PID:g601916
R:Bober, E.
submitted to the EMBL Data Library, January 1989
A:Reference number: S12458
A:Accession: S12458
A:Molecule type: mRNA
A:Residues: 785-1076, 'E', 1078-1123, 'A', 1125-1702, 'DE', 1705-1935 <BOB>
A:Cross-references: EMBL:X51591; NID:929467; PIDN:CAA35940.1; PID:929468
R:Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goede, H.W.; Arnold, H.H.
Eur. J. Biochem. 189, 55-65, 1990
A:Title: Identification of three developmentally controlled isoforms of human myosin hea
A:Reference number: S09331; MUID:90235862
A:Accession: S09331
A:Molecule type: mRNA
A:Residues: 785-830, 'X', 832-900, 'X', 902-970, 'X', 972-1040, 'X', 1042-1076, 'E', 1078-1110, 'X', 1104-1123, 'X', 1125-1158, 'C',
A:Cross-references: EMBL:X51591
R:Jandreski, M.A.; Llew, C.C.
Hum. Genet. 76, 47-53, 1987
A:Title: Construction of a human ventricular cDNA library and characterization of a beta
A:Reference number: S02229; MUID:87192738
A:Accession: S02229
A:Molecule type: mRNA
A:Residues: 1393-1702, 'DR', 1705-1935 <JAN>

A:Cross-references: EMBL:X06976; NID:g34860; PIDD:CAA30039.1; PID:g825694
R:Saetz, L.; Leinwand, L.A.
Nucleic Acids Res. 14, 2951-2969, 1986
A:Title: Characterization of diverse forms of myosin heavy chain expressed in adult h
A:Reference number: A93616; MUID:66176778
A:Accession: B23767
A:Molecule type: mRNA
A:Residues: 'LGVVELASG', 1311-1312, 'G', 1314-1355, 'R', 1357-1358, 'GD', 1361-1438, 'LQ', 14
A:Note: the first ten codons of the sequence figure show the reverse complementary st
C:Genetics:
A:Gene: GDB:MYH7
A:Cross-references: GDB:120215; OMIM:160760
A:Map position: 14q12-14q12
A:Introns: 67/3; 115/3; 168/1; 177/2; 213/3; 244/3; 266/1; 299/1; 333/3; 380/1; 419/3
24/3; 1390/2; 1451/3; 1507/3; 1548/3; 1651/3; 1719/3; 1761/3; 1853/3; 1930/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl
F:88-766/Domain: myosin motor domain homology <MOT>
F:178-185/Region: nucleotide-binding motif A (P-loop)
F:548-585/Region: actin binding #status predicted
F:655-677/Region: actin binding #status predicted
F:839-1935/Domain: coiled coil #status predicted <COI>
F:839-1279/Region: S2
F:1280-1935/Region: light meromyosin
F:129/Modified site: N6,N6,N6-trimethyllysine (lys) #status predicted
F:184/Binding site: ATP (lys) #status predicted
F:695,705/Active site: Cys #status predicted

Query Match 14.3%; Score 152.5; DB 1; Length 1935;
Best Local Similarity 20.5%; Pred. No. 0.47;
Matches 61; Conservative 60; Mismatches 88; Indels 89; Gaps 9;

QY 1 RTIINKLPEFDIAOEENVLDR-----EPLK----- 25
| : || || || : : : |
Db 1129 RAKVEKLKSDLSRELEETSERLEAGGATSVQIEMNKKREAEFOKMRRDLEATLQHEAT 1188
| : || || || : : : |
QY 26 -----NELDNVRAQLSOKDEKRDQYITDLRDTLEERNATVVSLOQA 69
| : || || : : : |
Db 1189 AALAKKHAADVAELGEQIDNLQRYVKQLEKESEFKLELDVATSNMQ-----IIRA 1241
| : || || : : : |
QY 70 LGAAMLCSTLKQKKYILEQOODETKQAQEEAGRLSRMKAT-----MQEILLQSQ 121
| : || || : : : |
Db 1242 KALEMKORTLEQDNEHRSKAEEFORSVNDLTSQRAKLQTEGELSRLDDEKALISQ 1300
| : || || : : : |
QY 122 LP-----EVEEIMRDMGVGQSAVEGLAYCYSLKKEYENLKEARKAGSEV 166
| : || || : : : |
Db 1301 LTRGLTYTTOOLEDLKRLQLEEBKAKNALAHALQSAHRDCCLLQBOYEETEAAEALQRV 1360
| : || || : : : |
QY 167 ADLKKRDLFFSSRSKLTQ---VSELDQAKLELSAQKDLQADAKELSLKKLTLMTQ 220
| : || || : : : |
Db 1361 LSKANSEVAQMQTKETETAIQRTTELEAKKLL-AQR-LQEAEEVAIVAKKCSLE 1415
| : || || : : : |

RESULT 23
S21801
myosin heavy chain, neuronal [similarity] - rat
N:Alternate names: myosin II
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: S21801; PNO013; S18134
R:Sun, W.; Chantler, P.D.
J. Mol. Biol. 224, 1185-1193, 1992
A:Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian br
A:Reference number: S21801; MUID:92235856
A:Accession: S21801
A:Molecule type: mRNA
A:Residues: 1-1199 <SUN>
A:Cross-references: EMBL:X62659
R:Sun, W.; Chantler, P.D.
Biochem. Biophys. Res. Commun. 175, 244-249, 1991
A:Title: A unique cellular myosin II exhibiting differential expression in the cerebr

Query Match	14.38;	Score 152;	DB 2;	Length 1175;
Best Local Similarity	23.98;	Pred. No. 0.3;		
Matches	62;	Conservative	49;	Mismatches 84;
				Indels 64;
				Gaps 9;

RESULT 26
A35815 myosin heavy chain 1, muscle - fruit fly (*Drosophila melanogaster*) (fragment)

C>Date: 12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 02-Feb-2001
 C/Accession: B32491
 R:George, E.L.; Ober, M.B.; Emerson Jr., C.P.
 Mol. Cell. Biol. 9, 2957-2974, 1989
 A:Title: Functional domains of the Drosophila melanogaster muscle myosin heavy-chain gene
 A:Reference number: A32491; MUID:89384556
 A:Accession: B32491
 A>Status: preliminary
 A:Molecule type: DNA; mRNA
 A:Residues: 1-2411 <GEO>
 A:Cross-references: GB:M61229; GB:M27194
 A>Note: the authors translated the codon TGC for residue 329 as Ser
 C:Genetics:
 A:Gene: FlyBase:Mhc
 A:Cross-references: FlyBase:FBgn0002741
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: ATP; nucleotide binding; P-loop
 F:137-1032/Domain: myosin motor domain homology #status atypical <MMO>
 F:227-234/Region: nucleotide-binding motif A (P-loop)

Query Match 14.3%; Score 152; DB 2; Length 2411;
 Best Local Similarity 23.9%; Pred. No. 0.63; Mismatches 84; Indels 64; Gaps 9;
 Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;
 QY 11 LAQEEENVLDREPLKNELDNVRAQLSOKDKER-----RDSQVYITDRLDTLE----- 57
 Db 1999 LEQENKYLRAQL---ELSQVROELDRRIQKEEFENTRNHQRALDSMASLEAEKKG 2055
 QY 58 -----ERNATVVSLOALGKAEMLCSTLKKOMKYLEQOODETKQAOEAGRLRSKM 108
 Db 2056 KAELRMKRLLEADINLELDHANKANAEQKNIRYQQLDIOQLALEEQGRARDA 2115
 QY 109 KTMQIEL-----LLOSQLEPEVEEMITDMGVGSVAQLAVCVSLKKEENLKEAKKA 162
 Db 2116 R--FOLGISERRANALQMLEESRTLEQADGRQABQ-----ELDAHEQOLNEVSAQ 2167
 QY 163 SGEVADKLKRDLFSSRSKLTQTVSELDQ-----AKL--ELKSAQKD 201
 Db 2168 NASSISAARK-----LESLQTLHSDLDLDELLEAKNSEKAKKAWDARLDELRAEDDH 2223
 QY 202 LOSADKEITMSLKKRLTLMQ 220
 Db 2224 AQTOEKLRKALEQOIKEIQ 2242

RESULT 30
 T17272
 hypothetical protein DKFZp434B0435.1 - human
 C:Species: Homo sapiens (man)
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
 C/Accession: T17272; T46451; A36881
 R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, September 1999
 A:Reference number: Z18723
 A:Accession: T17272
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1780 <POD>
 A:Cross-references: EMBL:AL117496
 A:Experimental source: adult testis; clone DKFZp434B0435
 R:Ansorge, W.; Winkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A:Reference number: Z23028
 A:Accession: T46451
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 575-1136, 'C', 1138-1608, 'K', 1610-1780 <AAA>
 A:Cross-references: EMBL:AL137392
 A:Experimental source: adult testis; clone DKFZp434I152
 R:Westendorf, J.M.; Rao, P.N.; Gerace, L.
 Proc. Natl. Acad. Sci. U.S.A. 91, 714-718, 1994
 A:Title: Cloning of cDNAs for M-phase phosphoproteins recognized by the MPW2 monoclonal

A:Reference number: A36881; MUID:94119956
 A:Accession: A36881
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1215-1261, 'E', 1263-1418, 'S', 1420-1608, 'K', 1610-1780 <WES>
 A:Cross-references: GB:L16782; NID:g292328; PIDN:AAC37542.1; PID:g292329
 C:Genetics:
 A>Note: DKFZp434B0435.1; DKFZp434I152.1
 C:Keywords: phosphoprotein

Query Match 14.2%; Score 151.5; DB 2; Length 1780;
 Best Local Similarity 21.3%; Pred. No. 0.49;
 Matches 50; Conservative 62; Mismatches 84; Indels 39; Gaps 6;
 QY 22 EFLKNELDNVRAQL-SQKD-----KEK-----RDSQVYITDRLDTLEERNAT----- 62
 Db 1039 EELDQLEKLAQAEVKGKVDENNRRLKEKKNQDDLEKEKTLIOQLKEELQEKVNTLDVQ 1098
 QY 63 --VVSLOALGKAEMLCSTLKKOMKYLEQOODETKQAOEAGRLRSKMKTMEIQLLQ 119
 Db 1099 IQHVEGKRALSELTQGYTCYKAKIKELETLLETKYVERSHALBODILEKESTILKLE 1158
 QY 120 SQRPEVEEMITDMGVGSVAQLAVCVSLKKEENL-----KEARKASGE 165
 Db 1159 RNLKEFQEHLDQ---SVKNTKDLNVKLELKEEITQLTNLQDMKHLLQLKEEETNRQ 1215
 QY 166 VADKLKRDLFSSRSKLTQTVSELDQAKLELSAQKDLOSADKEITMSLKKRLTLMQ 220
 Db 1216 ETEKLEELSSASARTONLQKADLQKEDVDLKEKITLDAKKQIKQYQEVSVNR 1270

RESULT 31
 S54871
 M protein - Streptococcus sp.
 C:Species: Streptococcus sp.
 C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
 C/Accession: S54871
 R:Podbielski, A.; Melzer, B.
 submitted to the EMBL Data Library, June 1991
 A:Reference number: S54871
 A:Accession: S54871
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-532 <POD>
 A:Cross-references: EMBL:X60097; NID:g840905; PIDN:CAAA2693.1; PID:g840906
 C:Superfamily: M5 protein

Query Match 14.2%; Score 151; DB 2; Length 532;
 Best Local Similarity 23.0%; Pred. No. 0.15; Mismatches 93; Indels 62; Gaps 8;
 Matches 62; Conservative 52; Mismatches 93; Indels 62; Gaps 8;
 QY 9 FDLAQOE-----EENVLDREPLK-----NELDNVRAQLS-----Q 37
 Db 174 YDLIEELGKRLKENQDLLEKTKDKEFYLGTLRYINELDLQGLNIDNLKHELEQ 233
 QY 38 KDKERDSQVYITDRLDTLEERNATVVSLOALGKAEMLCSTLKKOMKYLEQOODETKQ 97
 Db 234 KQKAEADQDT-LEAEKAKLEEEKQISDASRQSLRDLDSAREAKQLEAEYQKLEEEKQI 292
 QY 98 QEEAGR-LRSKMKTMEIQLLOSQLEPEVE-----MTRDMGVGSVAQLAV 145
 Db 293 SDASRQSLRDLDSAREAKQLEAEYQKLEQKNTISEASRGLRDLDSAREAKQYBKD 352
 QY 146 CVSLKKEENLKEARKASGEVADKLKRDLFSSRSKLTQTVSELDQAKLELSAQ---KDL 202
 Db 353 LANITAEIDKYKEERKQISDASRKGRLRDLDSAREAKQVEKALEANSKLALAKLKLKL 412
 QY 203 QSADK-----EIMSLKKLL 216
 Db 413 EESKRLTEKEKAELOAKLEAEKAKLEKL 441

RESULT 32
153799
CG1 protein - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I53799
R:Print, C.G.; Leung, E.; Harrison, J.E.; Watson, J.D.; Krissansen, G.W.
Gene 144, 221-228, 1994
A:Title: Cloning of a gene encoding a human leukocyte protein characterised by extensive
A:Reference number: I53799; MUID:94314220
A:Accession: I53799
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1300 <RES>
A:Cross-references: GB:I25616; NID:9409465; PIDN:AAB65853.1; PID:9409466
C:Genetics:
A:Gene: GDB:CG1
A:Cross-references: GDB:450341

Query Match 14.2%; Score 151; DB 2; Length 1300;
Best Local Similarity 26.6%; Pred. No. 0.38;
Matches 67; Conservative 40; Mismatches 81; Indels 64; Gaps 11;
QY 10 DLAGEENVLD--REFLNELDNVRAOLSOGRK-----E 41
DB 306 DLKESGVIODALKSSKGETLTHLOLEKDLAAVKEDAAATDRCKQLTQEMMTE 365
QY 42 KRDSQVIITLRLD--TLEE-----RNATVSLQOALGKAMLCSTLKKMKY---LEOQ 90
DB 366 KERNVAVITRKMDRIGTLEKEHNVFNKIHVSQO-----TQOMQKFFQVREOM 415
QY 91 QDETKOAEFGRLRSKM-KTMEIQLLOSQLPVEEMTRDAGVGOSAVQLAVYCSL 149
DB 416 EAETIAHLKQENGILRDVAVSNTTQLE--SKQSAELNKLKRDVYA--RLVNELEKTKGL 469
QY 150 KKEYENLEKARKASGEVADLRKDLFSSRSKLTQVYSELDOAKLELSAQKDLOS---A 205
DB 470 QQEEVQKKNMEQA---ATQLKVOLOEABERWEVOSYIRKRTAHEHRAQODLOSKEVAK 525
QY 206 DKEIMSLKKLTL 217
DB 526 ENEVQSLSKLT 537

RESULT 33
S24348
myosin heavy chain, embryonic and adult skeletal muscle (clone Comb2) - chicken (fragment
C:Species: Gallus gallus (chicken)
C>Date: 03-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
C:Accession: S24348
R:Moore, L.A.; Arrizubieta, M.J.; Tidymann, W.E.; Herman, L.A.; Bandman, E.
J. Mol. Biol. 225, 1143-1151, 1992
A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform
A:Reference number: S24348; MUID:92309413
A:Accession: S24348
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-955 <MOO>
A:Cross-references: EMBL:M74085
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament

Query Match 14.1%; Score 150.5; DB 2; Length 955;
Best Local Similarity 23.9%; Pred. No. 0.29;
Matches 56; Conservative 47; Mismatches 80; Indels 51; Gaps 8;
QY 24 LKNELDNVRAOLSOGRKDSQVIITLRLTLEERNATVSLQOALGKAMLCSTLKKQ 83
DB 222 LGEIDNLRVKOKLEKEKSELKMEIDDLASNME-----SVSKANLEKMKCRITLEDQ 274

QY 84 MKYLEQOODE-----TKQA--OEAGRL-----RSKMKTEQIETL 117
DB 275 LSKIKSKEEERQRMINDLSQARALQTESGEYSNOVEKDALISQSRGQAFQOIEEL 334
QY 118 LQSQLPEVEEMIRDMGVGOSAVQOLAVYCSLKKYEENLEAR-----KASGEVAD- 168
DB 335 KR-----HLEEFIRKAKNALAHALQSRHDCDLRQYEEDEQAKELQALSKANSEVAOW 390
QY 169 --KLRKLFSSRSKLTQVYSELDOAKLELSAQKDLOSADKEIMSLKKLTLMLQ 220
DB 391 RTKYETDAIGRTTELEAKKRLAQ--RLQDAEHEVAVNAKCAISLEKTRORLO 441

RESULT 34
B70356
chromosome assembly protein homolog - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Jun-2000
C:Accession: B70356
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666
A:Accession: B70356
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1156 <AQF>
A:Cross-references: GB:AE000699; NID:92983238; PIDN:AAC06839.1; PID:92983243; GB:AE00
A:Experimental source: strain VF5
C:Genetics:
A:Gene: xcpC
C:Superfamily: chromosome segregation protein SMCI

Query Match 14.1%; Score 150.5; DB 2; Length 1156;
Best Local Similarity 23.6%; Pred. No. 0.36;
Matches 52; Conservative 57; Mismatches 72; Indels 39; Gaps 9;

QY 11 LAQEEENVL-DREFLNELDNVRAOLSOGRKDSQVIITLRLTLEERNATVSLQOA 69
DB 232 LKKEKELKREKRIINLESLRESLEDITFQIDENKELEKRLERLLEKVEKIMPEREK 291
QY 70 LGR--AEMLCSTLKKQKYLEQOODETRKQAEAGRLRSKMKTEQIETLLOSQLPVEE 127
DB 292 VGRFTAE-----IENARSTIKEREKLESENRKYNLE--LNNLLSKEN 336
QY 128 MIRDGVGOSAVQOLAVYCSLKKYEENLEKARKASGEVADLRKDLFSSRSKLTQVYSE 187
DB 337 LEREVGLQLELEK-----LKREYSIKREVER-----EKLRL-ELLEBERLKITFDE 382
QY 188 L-----DQAKL--ELKSNQKDLQSDADKEIMSLKKLTLMLQ 220
DB 383 VKLEEEKELTKETKLSLNKEKQELQIQRANLKNKIERIK 422

RESULT 35
A47297
myosin heavy chain form B, nonmuscle - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Feb-2001
C:Accession: A47297; A55441
R:Bhatia-Dey, N.; Adelstein, R.S.; David, I.B.
Proc. Natl. Acad. Sci. U.S.A. 90, 2856-2859, 1993
A:Title: Cloning of the cDNA encoding a myosin heavy chain B isoform of Xenopus nonmu
A:Reference number: A47297; MUID:93219383
A:Accession: A47297
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1992 <BHA>
A:Cross-references: GB:L09740; NID:9214623; PIDN:AAA49915.1; PID:9214624
A:Experimental source: XTC cells
A:Note: sequence extracted from NCBI backbone (NCBIP:128722)

R:Kelley, C.A.; Oberman, F.; Yisraeli, J.K.; Adelstein, R.S.
 J. Biol. Chem. 270, 1395-1401, 1995
 A:Title: A Xenopus nonmuscle myosin heavy chain isoform is phosphorylated by cyclin-p34
 A:Reference number: A55441; MUID:95138137
 A:Accession: A55441
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 198-232 <KEL>
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: nucleotide binding; P-loop
 F:88-787/Domain: myosin motor domain homology <MOT>
 F:178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 14.1%; Score 150.5; DB 2; Length 1992;
 Best Local Similarity 22.9%; Pred. No. 0.63;
 Matches 58; Conservative 57; Mismatches 85; Indels 53; Gaps 9;

QY 4 INKLEFDLAQEEENV-----LDREF-----LKNELDNVRAQLSOK 38
 Db 1093 IEELKQLAKKEEELQALARQDEEVLOKNNMTLKVLELQAIQLQEDLESEKASRKKA 1152
 QY 39 DKERDSOVIIDTLQDTEERNATVSIQALGKRAEMLCSTLKKOMKYLEQOODETKQAQ 98
 Db 1153 EKQRDLSEELKTELEDLTDTTAAQOELTKREOEVAELRKS-----EETRNHE 1206
 QY 99 EAGRLRSGKMT-MEOIELLOSOLPEVEEMIRDMGVGSAVE-----OLAVYCVSLKK-E 152
 Db 1207 AIOQMRORQATALE-----LSEQLQAKRRVNIKKKOSLESNKELATEVKSLLQOK 1262
 QY 153 YENLKARKASGEV-----ADKLKRLDSSRSKSLQTVYSELQAKLELSAQKDLQ 203
 Db 1263 AESEKRRKRLGQVQELHAKVLEGRRLRADWVSKSKIQ---NELENVSLLEAKKGI 1319
 QY 204 SAKKEIHSLLKKL 216
 Db 1320 KLRDVASMESQL 1332

RESULT 36
 JCS837
 364K Golgi complex-associated protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 05-Mar-1998 #sequence.revision 13-Mar-1998 #text.change 20-Jun-2000
 C:Accession: JCS837
 R:Tokl, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Mismar, Y.; Ikehara, Y.
 Cell Struct. Funct. 22, 565-577, 1997
 A:Title: Identification and characterization of rat 364-kDa Golgi-associated protein rec
 A:Reference number: JCS837; MUID:98093490
 A:Accession: JCS837
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-3187 <TOK>
 A:Cross-references: DDBJ:D25543; NID:9516825; PIDN:BA05026.1; PID:9516826
 C:Comment: This protein plays a role in the formation and maintenance of the characteris
 C:Superfamily: giantin
 F:49-549,624-1176,1238-1707,1763-3114/Domain: coiled-coil leucine zipper #status predict
 F:3165-3187/Domain: membrane anchor #status predicted <MAD>

Query Match 14.1%; Score 150.5; DB 2; Length 3187;
 Best Local Similarity 19.0%; Pred. No. 1;
 Matches 58; Conservative 59; Mismatches 90; Indels 99; Gaps 7;

QY 10 DLAGEENVLDREFLKN---ELDNVRAQLSOKDKER-----DSQYIIDTLRPTLEER 59
 Db 1310 ELESSQLKADLEHLKTLQPLETLQKHVQKKEEVSYLVQLGKEKQTLTTVQTEMEQ 1369
 QY 60 NATVSL-----QALGKRAEMLCSTLKKOMKYLEQOQ----- 91
 Db 1370 ERLIKALHTQLEMQAKKEERLKOVOVEICELKKOPKEELSESKAKQOLQRKLQALALIS 1429
 QY 92 ---DETRQAQEEAGRLRSKM---KTMEQIELLQOSLPVEEMIRDMGVGSAVEOLA 143

Db 1430 KEALKENSLQEQSSARDVAEHLTKSLADVESQVYQNOEKDALGLKALLQDEERKLI 1489
 QY 144 V-----YCVSLK----- 150
 Db 1490 VEMDKSLLENQSLGSGCSLKLALQGLTDEKELKKELESVSCSIASSTEOEKHKLQ 1549
 QY 151 KEYENLKARKASGEVAKRLKRDLPFSSRSKSLQTVYSELQAKLELSAQKDLQSDKREIM 210
 Db 1550 KEYEVLLSYEVSNSEARIRQHVSVQEQEYAKLRSAESDKREKQLOQADQEME 1609
 QY 211 SLKKRL 216
 Db 1610 EKKEKKA 1615

RESULT 37
 S39082
 myosin heavy chain, embryonic - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 03-Feb-1994 #sequence.revision 03-Feb-1994 #text.change 13-Aug-1999
 C:Accession: S39082; S24349; A30170; S01265
 R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
 submitted to the EMBL Data Library, August 1991
 A:Description: Analysis of the chicken fast myosin heavy chain family: Localization o
 A:Reference number: S39081
 A:Accession: S39082
 A:Molecule type: mRNA
 A:Residues: 1-741 <MOO>
 A:Cross-references: EMBL:M74086
 A:Experimental source: clone Cem3
 R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
 J. Mol. Biol. 225, 1143-1151, 1992
 A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of 1sof
 A:Reference number: S24348; MUID:92309413
 A:Accession: S24349
 A:Molecule type: mRNA
 A:Residues: 1-12,14-741 <MOO2>
 A:Cross-references: EMBL:M74086
 A:Experimental source: clone Cem3
 R:Lagrutta, A.A.; McCarthy, J.G.; Scherzinger, C.A.; Heywood, S.M.
 DNA 8, 39-50, 1989
 A:Title: Identification and developmental expression of a novel embryonic myosin hea
 A:Reference number: A30170; MUID:89210285
 A:Accession: A30170
 A:Molecule type: DNA
 A:Residues: 723-741 <LAG>
 A:Cross-references: GB:M24691; NID:9341219; PIDN:AAA48950.1; PID:9531186
 R:McCarthy, J.G.; Heywood, S.M.
 Nucleic Acids Res. 15, 8069-8085, 1987
 A:Title: A long polypyrimidine/polyurine tract induces an altered DNA conformation o
 A:Reference number: S01265; MUID:88040428
 A:Accession: S01265
 A:Molecule type: DNA
 A:Residues: 723-741 <MCC>
 A:Cross-references: EMBL:X06251; NID:963600; PIDN:CAA29593.1; PID:963601
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; ATP; coiled coil; muscle

Query Match 14.1%; Score 150; DB 2; Length 741;
 Best Local Similarity 24.6%; Pred. No. 0.24;
 Matches 61; Conservative 46; Mismatches 81; Indels 60; Gaps 10;

QY 10 DLAGEENVLDREFLKNELDNVRAQLSOKDKERDSOVIIDTLRPTLEERNATVYSLQQA 69
 Db 3 DLSELELEI-----SEHLQVQKRL---EKESLKEIMIDLASNME-----SVSKA 46
 QY 70 LGKRAEMLCSTLKKOMKYLEQOODE-----TKQA--QDEAGRL----- 104
 Db 47 KANLEKMTETLEDLSLTKTEEEHQRMINDLNQRAQLQTEAGSYSNQVEEKDALISQL 106
 QY 105 -RSKMTWEQIELLQOSLPVEEMIRDMGVGSAVEQLAVYCVSLKKEYNLKEAR--- 160

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Db      107 SRGKAFVGGQIEELKRR-----HLEEETIKAKNLAHNLAAHLSGARHDCDLLRRQYEEEGCAKCEL 162
OY      161 -----KASGEVAD---KLRKDLFSSRSKLVYVSELDQAKLELKSQAQDLQADAKEINSL 212
Db      163 QRALSKANSEVAQWQRKTYETDAIQRTETEELKAKKTLAQ---RLQDAEEHVEAVNKAASL 219
OY      213 KKKLTLMLQ 220
Db      220 EKKQRLQ 227

RESULT 38
S02771
myosin heavy chain A [similarity] - Caenorhabditis elegans
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Caenorhabditis elegans
C:Date: 31-Dec-1993 #sequence_revision 19-May-2000 #text_change 19-Jan-2001
C:Accession: F23622; S02771
R:Harris, B.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19773
A:Accession: F23622
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1992 <MTL>
A:Cross-references: EMBL:Z78199; PIDN:CA01576.1; GSPDB:GN00023; CESP:K12F2.1
A:Experimental source: clone K12F2
R:DiBb, N.J.; Maruyama, I.N.; Krause, M.; Karn, J.
J. Mol. Biol. 205, 603-613, 1989
A:Title: Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gene
A:Reference number: S02771; MUID:89178677
A:Accession: S02771
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-116,140-1992 <DIB>
A:Cross-references: EMBL:X08067; MID:g6798; PIDN:CAA30856.1; PID:g6799
C:Gene: myo-3; CESP:K12F2.1
A:Map position: 5
A:Introns: 46/1; 192/1; 292/1; 468/2; 1921/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle co
F:89-807/Domain: myosin motor domain homology <MOT>
F:202-209/Region: nucleotide-binding motif A (P-loop)
F:690-712/Region: actin binding #status predicted
F:793-807/Region: actin binding #status predicted
F:875-1992/Domain: coiled coil #status predicted <COI>
F:875-1189/Region: S2
F:1190-1992/Region: light meromyosin
F:153/Modified site: N6,N6,N6-trimethyllysine (lys) #status predicted
F:208/Binding site: ATP (lys) #status predicted
F:730,740/Active site: Cys #status predicted

Query Match 14.1%; Score 150; DB 1; Length 1992;
Best Local Similarity 23.5%; Pred. No. 0.67;
Matches 64; Conservative 48; Mismatches 94; Indels 66; Gaps 10;

OY      5 NKLFLDLAGDEENNVDRFLKNELDNVRQLSQK-----DKEKRS 45
Db      921 NALFLSLFTEKANLADAEERNEKLQKLTATLESKLSIDITGOLEDNQERNEDLAROKKTD 980
OY      46 QVILDT-----LRDTLEE---RNATVYSLQALGAKMELCSLTKKQKYLEOOD 92
Db      981 QELSTTKKHVQDLESLTKRADEKQSRDHNIINSLODEMANQDEAVAKLKEKKH---QEE 1037
OY      93 ETKQAQEAEGRLSRKMKTMEOIETLLQSLQPEVEEMI---RDMGVGSAVQQLAVCVS 148
Db      1038 SNRKLTNEDLQSEEDKYNHLEKIRNKLQEQMDLEENIDREKSRSDIEKAKKVE---GD 1094
OY      149 LKKEVNELEKARKASGEVADKLK---DLFSSR-----SKLQVYVSL----- 188

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Db 1095 LKVAQENIDETLKQKHQVETLTKRKREEDLHHTNNKLAENNSIILAKDLRLKLTLARNAEL 1154

QY 189 -DQAKLELKSQAKDLQS---ADKEIMSLKKL 216

Db 1155 EEELEAFERNRSKOKSDRSRSEARELELTELRTL 1186

RESULT 39

S43354

plasmidogen-binding protein MLC72 - Streptococcus sp. (fragment)

C:Species: Streptococcus sp.

A:Variety: group G

C:Date: 07-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000

C:Accession: S43539; S43554

R:Ben Nasr, A.; Wistedt, A.; Ringdahl, U.

Eur. J. Biochem. 222, 267-276, 1994

A:Title: Streptokinase activates plasmidogen bound to human group C and G streptococci

A:Reference number: S43598; MUID:94291620

A:Accession: S43599

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-472 <BE2>

A:Cross-references: EMBL:Z32678; NID:9474769; PIDN:CA83589.1; PID:91333838

C:Superfamily: M5 protein

Query Match 14.0%; Score 149; DB 2; Length 472;

Best Local Similarity 24.7%; Pred. No. 0.17;

Matches 59; Conservative 46; Mismatches 94; Indels 40; Gaps 7;

QY 10 DLAGE-EENVLDREFLK-----NELDNVRAQLS-----OKDEKRDQVIT 49

Db 118 DLNOLDEKRLDKREFYLGSETLRYNELDLKLGOLINIDLKHLEDEKQKAEDRQT-L 176

QY 50 DTLRLTLERNATVSIQQAALGKAEMLCSTLKKMKYTLQEQDQTKQAQEEAGR-LRSM 108

Db 177 EAERKKELEERKQISDASKQSLRDLDSREAKKQLEAEYQAKLEERKQISDASKSLRDL 236

QY 109 KTMQEIQLLQSLPEVE-----MIRDMGVQSGAVQEDLAVYCVSLKREYENLK 157

Db 237 DASRAKKQLEAEYQKLEEQNKISASRSKGLRDLDSREAKKQ-----LEAHQKLE 289

QY 158 EARRAGSEVADLRKDLFSSRSKQLQTVYSELDQAKLELKSQAKDLQSADKEIMSLKKL 216

Db 230 EQNKISEASRSKGLRDLDSREAKKQVEKDLANLTAEIDKVAEERKQISDTSRSKGLRDL 348

RESULT 40

B72765

hypothetical protein APE0110 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 02-Feb-2001

C:Accession: B72765

R:Kikawadabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tanaka, H.; Takamizawa, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix

A:Reference number: A72450; MUID:99310339

A:Accession: B72765

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-919 <KAW>

A:Cross-references: DDBJ:AP000058; NID:95103388; PIDN:BAA79020.1; PID:95103499

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0110

C:Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match 14.0%; Score 149; DB 2; Length 919;

Best Local Similarity 23.1%; Pred. No. 0.34;

Matches 61; Conservative 52; Mismatches 83; Indels 68; Gaps 9;

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QY 12 AQEEENVLDR-EFLKNELDNVRAQLSQK----DKEKRDQVYIIDTLRDTLEERNATVYSL 66
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 410 SEKPESVLERLDAVINDLSEKARALDQEPASALEAEARLQALSMLESGSARCPCVCGA 469
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 QOALGKAEMLCSTLKKOMKYL----EQOODETKQAQEEAGRLRSKMKMTMEQIELLLQSQL 122
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 470 ELPPGRAEAIARHRYRHEERLKAAREKAAEAERASRLQDKRR--RIELL-SRL 525
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 PEVEEMIRDMGVQSAVQOLAVYCVSLKKEYENLKEARKASGEVADKLR----- 171
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 526 NQLEBGLRELGF--QTPEDLAKAEQKLMRLRLELELKLKLENSLEKVRNLSREVALRE 583
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 172 -----KDLFSSRSKLQ-----TVYSELQAK 192
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 584 AKTRALEVILQRLGIEKEEPAREKIKTLSSSESKLRLMLVSKAEDLATRLGITAYRSLDDL- 642
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 193 LELKSQOKDLOSADKEIMSLKKL 216
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 643 --LEKAREALEGVDEKELSAIERRL 664
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Search completed: September 4, 2002, 16:13:00
 Job time: 3244 sec